

#4

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humPMS2 (2574) 2661 2730
AtPMS2 (2267) 2661 2730
Consensus (2661) C TT CTCA A
humPMS2 (2587) ----
AtPMS2 (2337) ATGA
Consensus (2731)

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FIG. 1

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humPMS2	(1)	-----KRASSSS-----EPAKAKPIDRKS-----HSCSSQVLSLSTAVKELVENSLEAGATNDDL	70
AtMLH1	(1)	MIDSSSLTARYBEEESPATIVPREPPKQRLSESVNRAAEFIQRPVSAVKELVENSLEDDSSSSSV	
Consensus	(1)	ME ES AT I ID V I AG VI SAVKELVENSLEDA AS I L	
humPMS2	(57)	KLKRYVDLREVSNGCVBEENFEGLTKHHSFQIEADITQVETFSRGEASSELCAISD-----ISCH	140
AtMLH1	(71)	VVEGGLKCHQVSDDEHGIIRREDLPICERETTESLTKEDDFSLSSMFRGEASMTYVAH-----VTIT	
Consensus	(71)	LKD GL LI VSD G GI E L KH TSKI F DL L S GFRGEALASL LA VTIST	
humPMS2	(127)	ASAKVETLMDFHNGKIIQKTPYPRPRGTVS-----QOQSTLPVHEEFRIKKEDAMQVCHAYC-----ISA	210
AtMLH1	(141)	KGQIHETVSYRDGVMEHEPKACAAVKQOIMENSYNMIAFRITL-----SADDEGHIIDLSRMACHYN	
Consensus	(141)	G RL F KGT I V NLF L R K Q N DYAKIV LL I	
humPMS2	(197)	GIRVSTNQLGQKRPQVCTGGSSSIKENGGVFSQKQLQSIPFVQLPPSDSVCEEYGLSCSALHNL	280
AtMLH1	(210)	NVSFSRKH-----PAVKADHSVVSRLDSRSYYSVAKNM-----KV--E-----VSSC-----SSGCT	
Consensus	(211)	I SC G V S SPS D I SVFG LI L LS DA	
humPMS2	(267)	EYISGFSQCTHGVRSSDTRQFFENRPPCDPAKVCILVNEFHM-YNRHQYFFVLN-----SVDSCEVCH	350
AtMLH1	(264)	EDMEGFSNSNYVAKKTIL-----VLFTNDLVECSALKAEIETAAATLPKASKETVMSNLPREHVDL	
Consensus	(281)	F I GFSN H KS FIN R D A L R I VY K PFV L I L E VDIN	
humPMS2	(336)	VTDPRQIILQEEKLLAVLKTSLIGMFDSDVNKLNV-----QOPLLDVEGNLISMAHOLEKPMVEKODQSPS	420
AtMLH1	(331)	IHTKKEVSLNQEIIIIEMIQ-----SEVE-----VLRNNDTRTFQOKVEYIQ	
Consensus	(351)	I P KK I L III MI S IKL A K E	
humPMS2	(406)	LRTGEEKVSIKRLREAFSLRHTENKHSHPKTPEPRRSILQKRGMSSTSGAISDKGVLPQKEAF	490
AtMLH1	(377)	STLTSSSSSPVQKPSG-----QKQKQVKNMVRTDSSDAARLHAFQPKPQSLPDKVSSSVVRSSE	
Consensus	(421)	K D IS A T P P G A L L K AV	
humPMS2	(476)	SSSHGSDPTDRAETEKDSGHGSTSVDSSEGFSPDTGSHCSSEYAASPGDRSCSHHDSQEKAPETES	560
AtMLH1	(443)	RQRRNEKETACLSSQOE-----LIA--G-----V-DCCHFMLETRNCTYVGMADIV	
Consensus	(491)	P D D A V I S G E V DD	
humPMS2	(546)	ESLDCHSNQEDGCKFRVLPQPTNLATPNTDRFKKEEI-----SSSDICQKLVNTQDMSAQVDVAVKINKV	630
AtMLH1	(489)	EALQYN-----HLYLAN-----VVNLSELMYQQTERRFAHFNAIQLSDPAPISLILALKEEDL	
Consensus	(561)	FA V T SK L N I S S L L L	
humPMS2	(616)	VLDFSMSSAKKQQLHHQAQSEGSQNYRKRAKCPGENQADELKKEISKTFEAMEIIIGQFNLG	700
AtMLH1	(547)	DGNDTKDDKKEAEMNTLLKEKAMLEEYSVHEDSSAALSRLPVILDQYTPEDRVFPL-----LQCG	
Consensus	(631)	P S L RI L E AE F I N A I S M E I LG	
humPMS2	(686)	FIITKLNDIFIVDQHTDEKYNFEMLOQHTVLCQRLIAPQTINLTAVNEAVIELEIFRKNGF-----FVI	770
AtMLH1	(615)	NDVEWELKSCFQGVSAIGNFYAMHPPLPNPSDGIQFYSKRGESSQEKSDLECIVDMEDNLDQLLS	
Consensus	(701)	I E A F G I SA A L NLDI D L	
humPMS2	(756)	ENAPVTEAKLISLPTSKNTFGPDVDDELIFM-----SDSPGVMCPRSPQMFASRACRKSVMIGTALNTS	840
AtMLH1	(685)	ENAWAC-----EESIQHVLFPSMRLFKPPASMASNGTFPVASLEKLYKIFERC-----	
Consensus	(771)	D R WS L L M S VK K K	
humPMS2	(826)	EMKKLITHMGEMDHPWNCPHGRPTMRHIANLGVISON	877
AtMLH1	(738)	-----	
Consensus	(841)	-----	

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FIG. 3

humPMS2	(1)	1	70
AtPMS1	(1)	-----MTEKALPEGVRSMSRSLIIMFDMARVDEELAFNSLDAGATKVSIFVGVVSCS-VKIV	
Consensus	(1)	K IKPI H I SG IM LA V ELV NSLDAGAT I I L I V D	
humPMS2	(71)	71	140
AtPMS1	(59)	NGGVVEENFECS TLKHHS IQEADL-QVE-FCFGEALSLCALSDVTIS CHASAKVETELMFDH	
Consensus	(71)	G GV D L KH TSK DF LT ETFGFGEALASI IS L I T G R M	
humPMS2	(140)	141	210
AtPMS1	(129)	NGKIIQKTPYP-PP-RSTNSQQLSTLESHHEFERNISREYAKMVQVLHAYCTISAGI-----	
Consensus	(141)	I R GTTVSV LF S PVR K Q KK I L II A I	
humPMS2	(199)	211	280
AtPMS1	(199)	-----RPSCTNOLGQGRQPVVCGSPSIEKIIISV	
Consensus	(211)	EELPQTNPSSSAFLMRDAGTEAVNSLCKVNVTDGMLNVS GFECADDWPTDGOQGRNRRLQSIPYI	
humPMS2	(231)	281	350
AtPMS1	(269)	-----GQKQLQSLIPVQLPESDSVCEYEGSCSDALHNFYISCFISQCTHEVGRSSTRQF	
Consensus	(281)	LCIACPRRLYE SFEPKTHVEKKWCVLAFIRITANWKKDRIELFTGADILAKEDRQDLIDKI	
humPMS2	(290)	351	420
AtPMS1	(339)	FFIIR-----RPCDEAVVCLRVNEVYHMYNRHQYFFVVLNISVSECVDINTPDKRQIL	
Consensus	(351)	RLOGSSLSILHFLDADWPEAMERPKKLKRSNDHAPCSSLLFSADFQKQGYFSPRKDNVSPCEVE	
humPMS2	(346)	421	490
AtPMS1	(409)	QEEKLLAVLKTSLIGMFS DVNKLNVSCPLLEVEGNLIKMHADLEKPMVEEDQSPSLRGEKKDV	
Consensus	(421)	KIQNPKEQGTVAGFESRTD SLLQSRDIEMTNEFPQVTDLLETSLVADSKCRIFLTRCQITPVNINH	
humPMS2	(416)	491	560
AtPMS1	(479)	SISRLEAFS-----RRTTENKPHSKCTEPRRPLGQ	
Consensus	(491)	DFMKDSVDVLFQFQGLKDELVDVNCIGKHLRGCSSRVSLTFHEPKSEVEGYESVVMISNEKQSPRV	
humPMS2	(450)	561	630
AtPMS1	(549)	KRGMLSSITSGAISGVLRPQKEAVSSSHG--SDPTAEAEKDSGHGSSVSEGSIFITGSHCSS	
Consensus	(561)	LETREGGYCDVYSDPTDCSLGSSWQDTDWFTQCSSSGCGIGEDFNIPIPTABSDSYEKVGSKK	
humPMS2	(518)	631	700
AtPMS1	(619)	EYAASSPDRGSEQHVLSQ-----KAEETDDSFSDVDCHSNQEDTGCKFVRLCTNLATPNTKRFKE	
Consensus	(631)	YLSSVNVSSVTGSPCLSSWSPMYSTSATKWESEYQKGCRILEQSLRLGRMDEEFCSAANNIKFDH	
humPMS2	(583)	701	770
AtPMS1	(689)	SILSSSIQKLVNTQMSASQVDVVEVNEK---VVPLDFSMSSLAIRIKQLHHEAQSESEENYRK	
Consensus	(701)	EII D C S LA KI K L SI K QN G Q KK	
humPMS2	(649)	771	840
AtPMS1	(759)	PAKICPGENQ-----	
Consensus	(771)	PSAPPFYREKKRFISLCKSDTKPKNSDPSEPDDECLTQPCNASQMLKCSILDDVSYDHIQETEKRLS	
humPMS2	(659)	841	910
AtPMS1	(829)	SASDLKASAGCRTVHSETQDEVDHEDFSSEEFDPKISTTKWRHNCAVSQVPKESHELHGQDGVFDISSG	
Consensus	(841)		
humPMS2	(659)	911	980
AtPMS1	(899)	-----AASDELKESKIMFAEMEIIIGFNLGHITKLNEDIFVDCGHTDEKYNFEMQOHTVLOQRRL	
Consensus	(911)	LLHLRSDSLVPESNRHSLEDKVLQVDKKYPIVACGTVAVDCHADGRIRLEERTKFINALLI	
humPMS2	(724)	981	1050
AtPMS1	(969)	IAPQTLNITAVNEAVIENLIIFKNEFDFVDENAPVTERAK-----ISLSTSKNWTGPGQ	
Consensus	(981)	FVLTILKVPENGYQLQSYSEQIDWENICNITVEGSTSFQKQMSIIQRKPTPIITNAVECILGVNLSDV	
humPMS2	(782)	1051	1120
AtPMS1	(1039)	VDLIFMSSSPVMCRESRKQMFARCEKSVIITANTSEMKKLITHMGEMDHPWNPEGRFMR	
Consensus	(1051)	DL E I LADS G P V M SKACR AIM G AL SE II L FNC HGRPT	
humPMS2	(852)	1121	1164
AtPMS1	(1109)	HIANGVISQN-----	
Consensus	(1121)	PLVDEKALHKQIAKLSGRQVWHGLQRREITLDRAKSRLDNAKS-	
		I L I N	

FIG. 4

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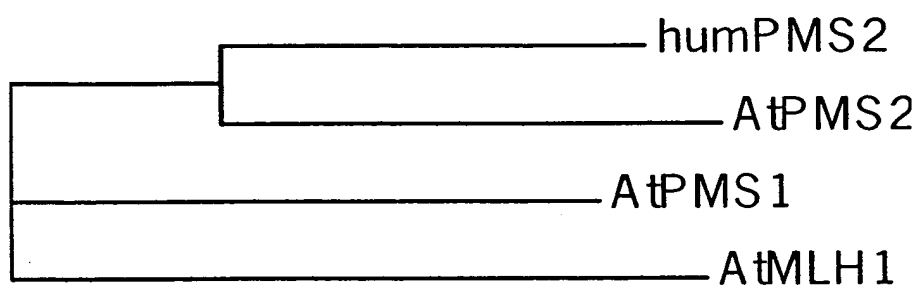


FIG. 5

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1
humPMS134 (1) ATGCGGAGCGGAGAGCTGGAGTACAGAACCTGTAAGGC-----ATCAACCTATGTCGGGTGT
AtPMS134 (1) ATGCGAGAGATCTTCTCTGCTCCGACGACCACTAGCTTTCCTTTGATAGACCTAAACAGAACCG
Consensus (1) ATG A GAG T CG T C CT CTA C AT A ACCTAT A G AA
71
humPMS134 (65) CAGCCATCAGATTCTCTGGCGGTGGACGAGTCTAAGCACTGGGTAAAGGAGTTAATAGAAAT
AtPMS134 (71) TGAATTCAGATCTCTTCGGTCAATCACTAGACCTCTCTTGGGCTCAAGGAGCTTCTCGAGAT
Consensus (71) A T CA AT TG TC GG CA GT T T CT C GC GT AAGGAG T GT GA AA
141
humPMS134 (135) CAGTTCGATGCTGGTCCCACTAATATGATCTAAGGCTAAGGACTTTCAGTGTCTTAAATGAGTT
AtPMS134 (141) TGGTTCGACGGCCGCCGACCGATATAGATTAACCCGAGACTTCCGCAATCTAATTCGGCTC
Consensus (141) AGTCT GA GC GG GCCAC A TAT GA T AA CT GACTA GG G GA T TT A GT
211
humPMS134 (205) TCAGTAAATGCAATGTGGG-----GAAGAA-----AAATTCGAAGGCTTAA
AtPMS134 (211) ATTGAATATGCTGTGGCAATTCGCCCAACCAATTTCTAGTTTGTGTCCAAATTCGGAAGAACTTTG
Consensus (211) GACAATGG TGTGG T A AAG AA CT CGAAG CTT
281
humPMS134 (251) -----CTTGGACATCACAGATCTAAGATCTAAGGTTGGCCCTAACTCGGTGCA-ACCT
AtPMS134 (281) ATGTTCTTCCACTTATCCAGCTTACTTCTAATATAGCGGTTTCAAGATTTT-CAATTTGCTACTT
Consensus (281) C CT AA CATCA AC TCTAA T A GA TT C GA CT T A TTGA ACTT
351
humPMS134 (311) TTGGCTTCGGGGGAATGCTCTGAGCTCAGTTGTGCTCTCAACGATGTCAACAATTCAGCTC--CC
AtPMS134 (350) ATGGTTTACAGGAGAGGCTCTGAGCTCTCCTGTGCTTTCGAAATCTCATGTGGAAACAAAGAAATA
Consensus (351) TGG TTT G GG GAAGC TGAGCTC CT TGTGCA TG G AT TCAC T AC G C A
421
humPMS134 (379) GATCCGCGAGCTTGGAAT---
AtPMS134 (420) GATGAGGCT---GTTGCTTGGCTC
Consensus (421) G AT GC A GTTG AC
444
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FIG. 6

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1
humPMS134 (1) --MERAESSSEPAKAKKIDKSVQICSGQVLSLSTAVKELVENSIDAGATNIDLKIKQVVLIE
AtPMS134 (1) MQGDSSFPITSSPLRFENENVIERICSGQVILSSAVKELVENSIDAGATSEINRDYGEYFO
Consensus (1) D A S ST A IKPI R IH ICSGQVIL LSSAVKELVENSIDAGAT IDI LKDYG D V
70
71
humPMS134 (69) SENGCCVEREN-----EGTLKHHTSHIQEADLTQVEFSGRGEALSSSLCALSDVVISCHA
AtPMS134 (71) IENGCCISPTNKVCVQILRRTFDVIALKHHTSHLEDTDLNLITYGFRGEALSSSLCALGNLVEVRTK
Consensus (71) DNGCGI NF D L LKHHTSKI DF DL NL TFGFRGEALSSSLCAL LTI T
140
141
humPMS134 (128) SAKIG
AtPMS134 (141) NEPIA
Consensus (141) VAT
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FIG. 7

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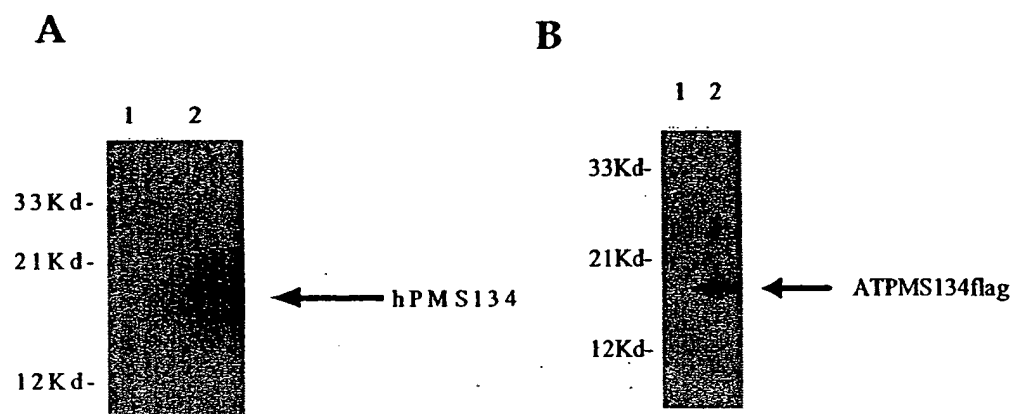


FIG. 8

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T090-T0964260

Dominant Negative Effects of *Arabidopsis thaliana* PMS2 homolog

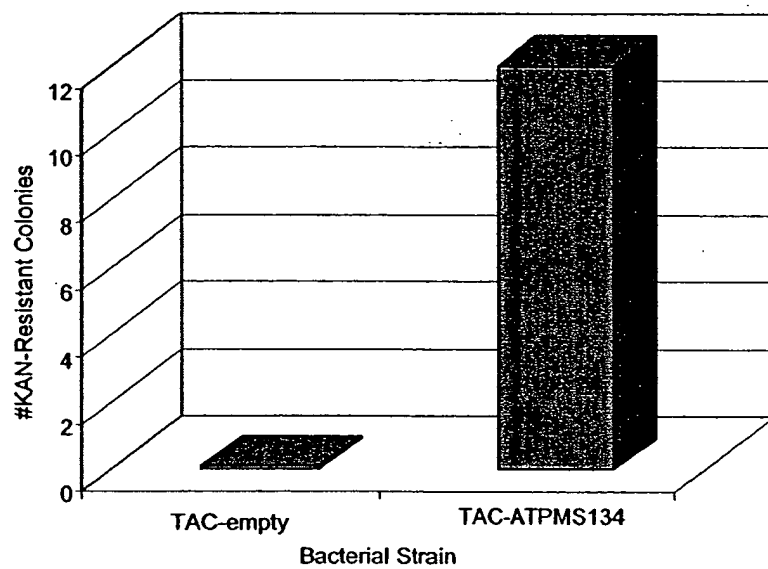


FIG. 9

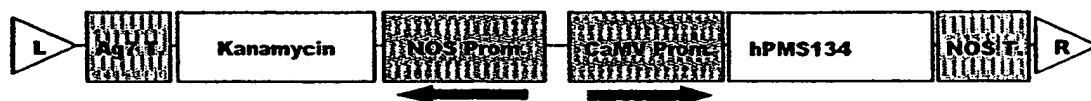


FIG. 10

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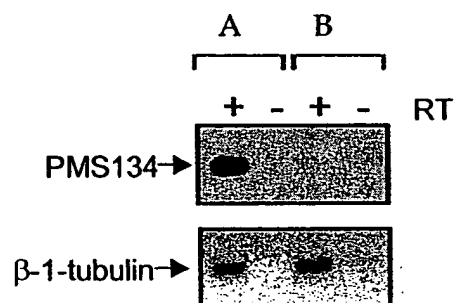


FIG. 11

A= PMS134 expressing plants
B= pBI-121 control plants

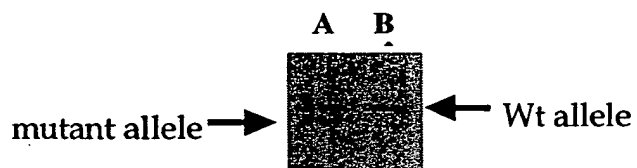
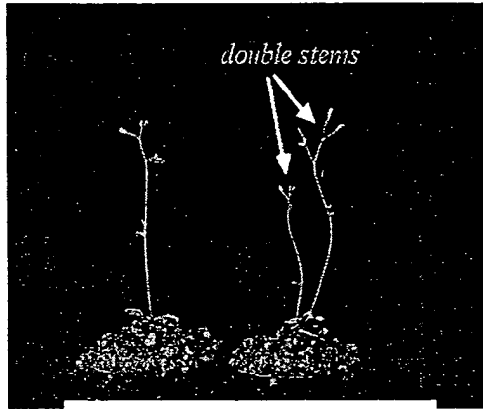


FIG. 12

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Normal MMR-

FIG. 13